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indicates a conservative substitution. The cysteine-rich portion of the consensus sequence (SEQ ID NO: 13) appears in boldface.

Figures 12A and 12B show the sequence of hTACI (SEQ ID NO: 14). TACI's extracellular domain (SEQ ID NO: 15) extends from aa 1 to aa 166. The cysteine-rich consensus region (SEQ ID NO: 16) is shown in boldface, and the transmembrane region (SEQ ID NO: 17) is underlined. hTACI-Fc (SEQ ID NO: 18).

Figure 13 shows an alignment of cysteine rich extracellular regions of human TACI and human BCMA. The BCMA cysteine rich consensus region (SEQ ID NO: 20) appears as the top line, the TACI cysteine rich consensus region (SEQ ID NO: 21) appears as the bottom line of each row. Conserved amino acid residues are indicated by a vertical bar (I). Related amino acid residues are indicated with a colon (:).

Figures 14A, 14B and 14C show soluble mouse G70/APRIL binding to 293 cells expressing the BCMA gene. Human 293 cells transfected with the pmBCMA and pcDNA3 vectors were incubated with G70/APRIL-Flag, followed by FITC-conjugated anti-Flag antibody staining for FACS analysis. A. 293 cells transfected with pcDNA3 vector only. B. 293 cells transfected with antisense pmBCMA vector. C. 293 cells transfected with sense pmBCMA vector.

Table 2 shows BIACore analysis of the stoichiometric binding kinetics of APRIL and AGP-3 to BCMA and TACI. Flag-APRIL specifically binds to murine and human BCMA with affinities of 0.25 nM and 0.29 nM, respectively, and to human TACI with an affinity of 1.48 nM. Also a longer version of Flag-tagged APRIL (aa 50-240) binds to BCMA and TACI with high affinity similar to that of Fc-AGP-3 (Table 2). In separate experiments, we determined that neither APRIL nor AGP-3 bind to OPG and also that TNFα, OPGL, LIGHT, TWEAK, and TRAIL do not